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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/555,529	07/24/2000	PATRICIA KANNOUCHE	192863US0PCT	6934
22850	7590	03/06/2006	EXAMINER	
OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. 1940 DUKE STREET ALEXANDRIA, VA 22314			JOHANNSEN, DIANA B	
		ART UNIT	PAPER NUMBER	
		1634		

DATE MAILED: 03/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/555,529	KANNOUCHE ET AL.	
	Examiner	Art Unit	
	Diana B. Johannsen	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).

Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) Responsive to communication(s) filed on 01 September 2005.
- 2a) This action is FINAL. 2b) This action is non-final.
- 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) Claim(s) 30-78 is/are pending in the application.
- 4a) Of the above claim(s) 43-58,66-73 and 75-78 is/are withdrawn from consideration.
- 5) Claim(s) _____ is/are allowed.
- 6) Claim(s) 30-42,59-65 and 74 is/are rejected.
- 7) Claim(s) _____ is/are objected to.
- 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) The specification is objected to by the Examiner.
- 10) The drawing(s) filed on _____ is/are: a) accepted or b) objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. _____.
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)	4) <input type="checkbox"/> Interview Summary (PTO-413)
2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)	Paper No(s)/Mail Date. _____.
3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date <u>0203</u> .	5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)
	6) <input checked="" type="checkbox"/> Other: <u>sequence alignments</u> .

FINAL ACTION

1. This action is responsive to the complying complete set of claims filed 01 September 2005, as well as to the Supplemental Response to Election of Species filed 30 September 2003. Any rejections not reiterated in this action have been withdrawn.

This action is FINAL.

2. It is noted that the new title and amendments to the specification filed 15 July 2004 (and re-submitted 01 September 2005) have been entered.

Election/Restriction

3. It is again noted that the Amendment of 10 February 2003 canceled original claims 1-29 (which claims were subject to the Restriction Requirement mailed 08 July 2002), and added new claims 30-78. New claims 30-42, 59-65, and 74-75 are drawn to nucleic acids encoding proteins and fragments thereof, expression vectors, host cells, and nucleic acid detection reagents, and therefore correspond to elected Group I.

4. Newly submitted claims 43-58, 66-73, and 76-78 are directed to inventions that are independent or distinct from the invention originally claimed and elected by Applicant (see the Response to Restriction Requirement filed 08 August 2002) for the following reasons:

-New claims 43-53, 66-73, and 76-78 are drawn to methods for detecting nucleic acids, corresponding to non-elected Group II (original claims 6-12); and

-New claims 54-58 are drawn to methods in which polynucleotides are expressed in cells so as to produce proteins that inhibit cell proliferation, corresponding to non-elected Group VI (original claim 26).

Applicant has received an action on the merits for the originally presented and elected invention of Group I. As the inventions of claims 43-58, 66-73, and 76-78 correspond to non-elected inventions previously withdrawn from consideration, claims 43-58, 66-73, and 76-78 are also withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

5. Additionally, Applicant's election with traverse of SEQ ID Nos 18, 19, 27, and 28 in the reply filed on 06 June 2003 is acknowledged. The traversal is on the ground(s) that the Office "has not provided adequate reasons and/or examples to support a conclusion of patentable distinctness between the identified groups." The response continues that the statement by the examiner that "each primer pair is characterized by a different combination of particular nucleotide sequences and functions in the amplification of a different target sequence" is "an unsupported conclusion." This is not found persuasive because applicants' own specification provides the sequences of each primer (each of which differs from the other) and exemplifies the fact that each primer pair amplifies a different target sequence, such that the examiner's conclusion is supported by the teachings of applicants' own specification. Further, Applicants' response has provided no specific arguments supporting a conclusion different from that reached by the examiner (for example, applicants have not indicated what they believe might constitute a "special technical feature" shared by all the molecules encompassed by the claims). Accordingly, Applicants' arguments are not persuasive.

The requirement is still deemed proper and is therefore made FINAL.

It is noted that in the Supplemental Response of 30 September 2003, Applicant clarified the fact that claims 45, 48, 49, 68, 71, 74, 76, and 77 read on the elected primers. Of these claims, only claim 74 is encompassed by elected Group I.

Claim 75, which is encompassed by Group I, does not read on elected primers SEQ ID NOS 18, 19, 27 and/or 28. Accordingly, claim 75 is withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 06 June 2003.

Claim 74 is also withdrawn from consideration to the extent that it is drawn to non-elected sequences (i.e., sequences other than elected primers SEQ ID Nos 18-19 and a "fragment obtained by amplification of a kin17 nucleotide sequence with SEQ ID NO: 18 and SEQ ID NO: 19").

6. This application contains claims 43-58, 66-73, and 75-78 drawn to inventions nonelected with traverse. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144). See MPEP § 821.01.

7. Applicants' request in the response of 10 February 2003 that non-elected process claims be rejoined at such time as the elected claims are found allowable is noted. However, no claims are allowed at this time.

Declaration under 37 CFR 1.132

8. In view of the cancellation of original claims 1-5, 24-25 and 29, it is noted that the rejections of those claims set forth in the Office action of 09 October 2002 are moot.

However, it is also noted that the Declaration under 37 CFR 1.132 filed 10 February 2003 is sufficient to disqualify the Kannouche et al reference (Biochimie 79:599-606 [1997]) as prior art under 35 USC 102(a).

Information Disclosure Statement

9. The information disclosure statement filed 10 February 2003 fails to comply with 37 CFR 1.98(a)(2), which requires a legible copy of each cited foreign patent document; each non-patent literature publication or that portion which caused it to be listed; and all other information or that portion which caused it to be listed. Specifically, no copy of reference AAA (M.D. Adams et al) has been provided; accordingly, that reference has not been considered.

Claim Rejections - 35 USC § 112

10. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED

BY APPLICANTS' AMENDMENTS TO THE CLAIMS

11. Claims 39-42 and 64-65 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a new matter rejection.

While applicants' specification discloses bacteria and particular lines of cells comprising vectors and plasmids that express various kin17 proteins and variants thereof (see, e.g., page 1 and examples throughout the specification), the specification as originally filed does not broadly disclose host cells comprising polynucleotides that encode such proteins, as encompassed by the instant claims. The specification does not refer to or provide any type of limiting definition of the term "host cell," and the claims as written are sufficiently broad so as to encompass any type of cell comprising the claimed polynucleotides in any form (including polynucleotides which are [unlike the molecules exemplified in the specification] free of any type of vector or plasmid construct). It is noted that Applicants have not provided any type of specific reference to locations in the specification that are believed to provide basis for the claims (rather, Applicants merely state that support is found "in Claims 1-29 and the specification as originally filed" (see the response of 10 February 2003)), and the examiner could not identify basis for this subject matter as it is now broadly claimed. Accordingly, claims 39-42 and 64-65 introduce new matter.

12. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

**THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY
APPLICANTS' AMENDMENTS TO THE CLAIMS**

13. Claims 30-42 and 59-65 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 30-42 and 49-65 are indefinite over the recitation of the language "kin17 protein which comprises an amino acid sequence wherein amino acids ____ to ____ are deleted in SEQ ID NO:____" in claims 30, 32-34, and 59-60. This language does not make clear the structural requirements of the molecules encompassed by the claims. While the claims make reference to particular amino acids that are "deleted in" a SEQ ID NO, the claims do not otherwise require that the "non-deleted" portion of that SEQ ID NO be present in the claimed molecules. While one of skill in the art could clearly identify a molecule comprising, e.g., the two portions of SEQ ID NO: 26 flanking a particular "deleted" region, it is not clear how one would or could identify molecules encompassed by the claims that do not include the "non-deleted" portion of the SEQ ID NO referenced in the claims. Clarification is required.

Claim Rejections - 35 USC § 101

**THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY
APPLICANTS' AMENDMENTS TO THE CLAIMS**

14. 35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

15. Claims 39 and 65 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims do not sufficiently distinguish over cells that exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring

products are considered non-statutory subject matter. See *Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980).

Specifically, instant claims 39 and 65 as written encompass cells found in nature that comprise wild-type kin17 molecules. While it is noted that claims 31 and 61 (from which claims 39 and 65, respectively, depend) are drawn to “isolated” polynucleotides, as claims 39 and 65 are drawn to host cells that “comprise” such polynucleotides, the polynucleotides encompassed by claims 39 and 65 are not “isolated” molecules.

(With regard to claims 40-42 and 64 (which are also drawn to “host cells”), it is noted that as the host cells of these claims comprise deletion constructs that are not found in nature, these claims meet the requirements of 35 USC 101.)

Claim Rejections - 35 USC § 102

**THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY
APPLICANTS' AMENDMENTS TO THE CLAIMS**

It is noted that while applicants' claims previously encompassed nucleic acid fragments of SEQ ID NO: 1 consisting of SEQ ID NO: 18 or SEQ ID NO: 19 (see, e.g., original claim 5), as well as a group of reagents including SEQ ID NO: 18 and SEQ ID NO: 19 (in combination with several other reagents; see, e.g., original claim 29), instant claim 74 encompasses both an isolated polynucleotide comprising SEQ ID NO: 18 and an isolated polynucleotide comprising SEQ ID NO: 19.

16. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

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(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

17. Claim 74 is rejected under 35 U.S.C. 102(b) as being clearly anticipated by

Matsuda et al (The Journal of Biological Chemistry 268(33)24950-24958 [1993]).

Matsuda et al disclose double-stranded vectors comprising instant SEQ ID NO:

18 (see entire reference, particularly the "Materials and Methods" section at pages 24950 and Figure 3, particularly nucleotides -270 through -249, which are the reverse complement of instant SEQ ID NO: 18). Accordingly, Matsuda et al clearly anticipate the claimed invention.

18. Claim 74 is rejected under 35 U.S.C. 102(a) as being clearly anticipated by EST database accession no. AI089251 (NCI-CGAP; gb09a11.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone, 8/1998).

EST database accession no. AI089251 discloses a cDNA comprising instant SEQ ID NO : 19 (see entire reference, particularly nucleotides 218-243 of the sequence). Accordingly, EST database accession no. AI089251 clearly anticipates the claimed invention.

Conclusion

19. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure. Sequence alignments are provided to show the identity shared between the nucleic acid of Matsuda et al and instant SEQ ID NO: 18, and the nucleic acid of EST database accession no. AI089251 and instant SEQ ID NO: 19.

20. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

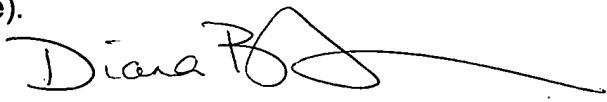
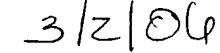
A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Diana B. Johannsen whose telephone number is 571/272-0744. The examiner can normally be reached on Monday and Thursday, 7:30 am-4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached at 571/272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


Diana B. Johannsen
Primary Examiner
Art Unit 1634


Sequence alignments

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 12:53:47 ; Search time 116.932 Seconds
(without alignments)
10624.773 Million cell updates/sec

Title: US-09-555-529-18

Perfect score: 22

Sequence: 1 agaaagtgtatcgctggcggtt 22

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenBank;*
2: gb_ba;*
3: gb_in;*
4: gb_env;*
5: gb_ov;*
6: gb_dat;*
7: gb_ph;*
8: gb_pr;*
9: gb_ro;*
10: gb_stai;*
11: gb_sy;*
12: gb_uni;*
13: gb_vir;*
14: gb_hg;*
15: gb_pl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	ALIGMENTS
1	22	100.0	22	6 AX003325	AX003325 Sequence	1	AX003325	Sequence 18 From Patent WO9929845.	W09929845.	22 bp	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
2	22	100.0	1002	6 AX003310	AX003310 Sequence	2	AX003310	Sequence 100.0% Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CQ722054 Sequence	100.0%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
3	22	100.0	1117	6 CQ722054	CQ722054 Sequence	3	CQ722054	Sequence 100.0% Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AX003308 Sequence	100.0%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
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7	22	100.0	174351	8 AL158044	AL158044 Sequence	7	AL158044	Sequence 100.0% Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AL158044 Human DNA	100.0%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
8	22	100.0	194563	14 AL1591687	AL1591687 Sequence	8	AL1591687	Sequence 100.0% Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AL1591687 Homo sapiens	100.0%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
9	18.4	83.6	7111	14 AC017711	AC017711 Sequence	9	AC017711	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Danio rerio	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
10	18.4	83.6	166348	14 CRB47851	CRB47851 Sequence	10	CRB47851	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Danio rerio	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
11	18.4	83.6	166906	5 AC16480	AC16480 Sequence	11	AC16480	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Danio rerio	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
12	18.4	83.6	170597	5 AL929558	AL929558 Sequence	12	AL929558	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Zebrafish	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
13	18.4	83.6	177953	2 AC018491	AC018491 Sequence	13	AC018491	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Drosophila	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
14	18.4	83.6	297848	2 AB02611	AB02611 Sequence	14	AB02611	Sequence 83.6% Score 22; DB 6; Length 22; Best Local Similarity 83.6%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Drosophila	83.6%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
15	17.8	80.9	460	1 AY525807	AY525807 Sequence	15	AY525807	Sequence 80.9% Score 22; DB 6; Length 22; Best Local Similarity 80.9%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Streptococcus	80.9%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
16	17.8	80.9	889	5 BX931015	BX931015 Sequence	16	BX931015	Sequence 80.9% Score 22; DB 6; Length 22; Best Local Similarity 80.9%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Gallus gallus	80.9%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
17	17.8	80.9	2169	5 CR382725	CR382725 Sequence	17	CR382725	Sequence 80.9% Score 22; DB 6; Length 22; Best Local Similarity 80.9%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Gallus gallus	80.9%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence
18	17.8	80.9	6584	3 AY236226	AY236226 Sequence	18	AY236226	Sequence 80.9% Score 22; DB 6; Length 22; Best Local Similarity 80.9%; Pred. No. 18; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Unculture	80.9%	DNA	linear	PAT 24-AUG-2000	AB005005 Halobacter AC150077 Gallus ga Continuation 9 of I23942 Escherichia U49647 Escherichia ED247478 Variant E AR408798 Sequence X67470 E. coli AMS AR061799 Hydroлагу D90744 Escherichia Continuation (4 of Continuation (1223 Continuation (223 AC060755 Oryza sat AC078469 Sequence CQ078469 Sequence CQ109433 Sequence CQ148085 Sequence CQ183469 Sequence CQ207864 Sequence CQ231346 Sequence CQ269518 Sequence CQ306575 Sequence CQ343626 Sequence

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TDWLOPBTIVKIKTRKGKGEKTHKKKAVKVEVDKTYTAWVMQDMSDKDQDTHLT
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A"

ORIGIN

Query Match Score 22; DB 8; Length 1528;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	AGAAAGTGATCGCTGCCGGT	22
40	AGAAAGTGATCGCTGCCGGT	61

RESULT 6

HUMATPGC HUMATPGG 23065 bp DNA linear PRI 13-FEB-2003
 DEFINITION Homo sapiens gene for ATP synthase gamma-subunit, complete cds.
 ACCESSION D16561
 VERSION D16561.1
 KEYWORDS GI:468446

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Homidae; Homo

REFERENCE 1 (bases 1 to 23065)

AUTHORS Matsuda,C., Endo,H., Ohta,S. and Kagawa,Y.

TITLE Gene structure of human mitochondrial ATP synthase gamma-subunit. Tissue specificity produced by alternative RNA splicing

JOURNAL J. Biol. Chem. 268 (33), 24950-24958 (1993)

PUBMED 822057

REFERENCE 2 (bases 1 to 23065)

AUTHORS Kagawa,Y.

TITLE Direct Submission

JOURNAL Submitted (23-JUN-1993) Yabuo Kagawa, Jichi Medical School, Department of Biochemistry, 3311-1 Yakuishi, Minamikawachi-machi, Tochigi 329-0498, Japan (E-mail:ykagawa@dbj.nig.ac.jp), Tel:81-285-44-2111(ex.3149), Fax:81-285-44-1827

FEATURES Location/Qualifiers

SOURCE 1. . 23065

/organism="Homo sapiens"

/mol_type="genomic DNA"

/tissue_type="blood"

/clone_id="lambda dash II"

/note="clones harpg[2, 5, 21 and 23]"

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CDS /number=1

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 14839..14982,15094..15158,17329..17484,17817..17913,
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/note="H(heart)-type ATP synthase gamma-subunit"

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/product="ATP synthase gamma-subunit"

/protein_id="BA0394_1"

/db_xref="GI: 665584"

TRANSLATION="MFRAGVAGLISANTLQPWQIVENMATLDIRTRKSIKNIQKI
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 CGKHSIAKQMKSEPAVLLTAAGKEVMLVGLGDKIRLYRHSDOPLVKERKEVSKP
 PTGFDASVIALBLINSYFEDGSIIFNPKFSVISYKTEPEKPIESINTVADHSIY
 DDIDAVYDQYQYNNYLSKSTTSOSARTAMONASNSKNSMIDKLFN
 RTRQAVITKEJIEISGAL"
 JOIN(4219..4274,11169..11203,12114..12245,14057..14261,
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/note="L(liver)-type ATP synthase gamma-subunit"
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  PTGFDASVIALBLINSYFEDGSIIFNPKFSVISYKTEPEKPIESINTVADHSIY  

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  RTRQAVITKEJIEISGAL"  

  RTQAVITKEJIEISGAL"

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ORIGIN

Query Match Score 22; DB 8; Length 23065;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	AGAAAGTGATCGCTGCCGGT	22
Db	3970	AGAAAGTGATCGCTGCCGGT	3949

RESULT 7

ALL58044/C ALL58044 174361 bp DNA linear PRI 18-MAY-2005
 DEFINITION Human DNA sequence from clone RP1-264C14 on chromosome 10 Contains the 5' end of the gene for a novel protein (MCC1084), the ITIH2 gene for inter-alpha (globulin) inhibitor, H2 polypeptide (H2P), the KIN gene for KIN, antigenic determinant of rcaA protein homolog (mouse), the 3' end of the ATP5C1 gene for ATP synthase, H⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C, ATP5CL), a novel gene and two CpG islands, complete sequence.

ACCESSION ALL58044

Run on: November 26, 2005, 12:58:53 ; Search time 145,336 Seconds
 OM nucleic - nucleic search, using sw model

Post-processing:	Minimum Match 0%	Maximum Match 100%
Database :	EST*	
	1: gb_est1:*	
	2: gb_est2:*	
	3: gb_est3:*	
	4: gb_htc:*	
	5: gb_est4:*	
	6: gb_est5:*	
	7: gb_est6:*	
	8: gb_est7:*	
	9: gb_gsb1:*	
	10: gb_gsb2:*	
	11: gb_gsb3:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	26	100.0	249	AI493544
2	26	100.0	328	BE991046
3	26	100.0	384	AK770446
4	26	100.0	384	AI493563
5	26	100.0	386	BM661987
6	26	100.0	469	AI087818
7	26	100.0	476	AI7378396
8	26	100.0	485	AI089251
9	26	100.0	488	BM689918
10	26	100.0	512	BQ548883
11	26	100.0	516	BG344189
12	26	100.0	521	BE349628
13	26	100.0	543	CB158644
14	26	100.0	575	BW50112
15	26	100.0	591	BB96845
16	26	100.0	592	CX066354
17	26	100.0	605	CB242699
18	26	100.0	660	AL597250
19	26	100.0	682	AV721396
20	26	100.0	698	AI650375
21	26	100.0	701	AI807250
22	26	100.0	720	CX01009

Scoring table: IDENTITY_NUC Gap=10.0 , Gapext 1.0

Searched: 41070325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

ALIGNMENTS

RESULT	1
LOCUS	AI493544
DEFINITION	th36310.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120346 3' mRNA sequence.
ACCESSION	AI493544
VERSION	AI493544.1
KEYWORDS	EST
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Homidae; Homo.
REFERENCE	1 (bases 1 to 249)
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE	Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov
FEATURES	DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINN at: www-bio-linl.gov/bbfp/image/image.html Insert Length: 841 Std Error: 0.00 Seq Primer: -40bp from Gibco High quality sequence stop: 246. Location/Qualifiers 1..249 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMGR:2120346" /tissue_type="adenocarcinoma" /lab_host="DH10B" /clone_libr="NCI CGAP Pan1" /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; Sali; Site: 2; Note: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
ORIGIN	Query Match Score 26; DB 1; Length 249; Best Local Similarity 100.0%; Pred. No. 0.42;

the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHP pool 1; 309384-310919, 33208-32895 Soares Nb2HP pool 1; 145032-147335, 147720-148103, 148872-14925, 15002 - 150407, 151176-152327 Soares Nb2HFR-3W pool 1; 758280-760583, 772104-774407 Soares NbHPA pool 1; 304776-306311, 320136-322823, 326280-326663 Soares NbHOR pool 1; 72372-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 100.0%; Score 26; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.46; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 231 GCGAACACCAATTGATCTTAAAGA 256

RESULT 7

AI378396 Al378396 AI378396 tc7ff05_x1 Soares_NbHMPU_S1 Homo sapiens mRNA linear EST 18-MAR-1999 476 bp mRNA cDNA clone IMAGE:2070753

DEFINITION t7ff05_x1 Soares_NbHMPU_S1 Homo sapiens mRNA linear EST 18-MAR-1999 476 bp mRNA sequence.

ACCESSION Al378396

VERSION Al378396.1 GI:4188249

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

COMMENT

CONTACT

E-mail: cgabp-r@mail.nih.gov

This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq. primer: -40m3 fwd. BT from Amersham

High quality sequence stop: 442.

FEATURES

SOURCE

ORGANISM

COMMENT

CONTACT

E-mail: cgabp-r@mail.nih.gov

This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq. primer: -40m3 fwd. BT from Amersham

High quality sequence stop: 442.

LOCATION/Qualifiers

1. .485

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1695740"

/sex="female"

/dev_stage="adult"

/clone_lib="Soares_pregnant_uterus_nbhpu"

/notes="Organ: uterus; Vector: pT73-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-ACTGGAGAGTCGCCGCTTTTTTTTTT 3']"

/clone_host="DH10B"

/db_xref="taxon:9606"

/clone="IMAGE:2070753"

/tissue_type="pooled human melanocyte, fetal heart, and pregnant uterus"

/lab_host="DH10B"

/clone_lib="Soares_NbHMPU_S1"

/notes="Organ: mixed (see below); Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NbH19W) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 26032-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 100.0%; Score 26; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 218 GCGAACACCAATTGATCTTAAAGA 243

RESULT 9

BM689918/BM689918

DEFINITION UI-E-CKL-abo-f-09-0-UI r1 UI-E-CKL Homo sapiens mRNA linear EST 28-FEB-2002 488 bp mRNA sequence.

ACCESSION BM689918

VERSION BM689918.1 GI:19903176

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

COMMENT

JOURNAL

REFERENCE

AUTHORS

Bonaldo, M.P., Lennon, G. and Soares, M.B.

ORIGIN

Query Match 100.0%; Score 26; DB 1; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.46; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCGAACACCAATTGATCTTAAAGA 26

1 GCGAACACCAATTGATCTTAAAGA 26